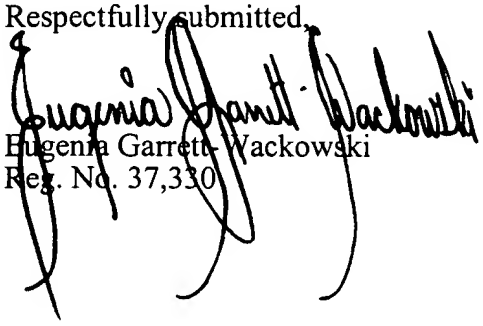
If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,



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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Paragraph **[24]** beginning at line 7 of page 7 has been amended as follows:

[24] FIGURE 1. Genomic structure (A), putative topology (B), and predicted amino acid sequences of *ABCG5* (SEQ ID NO:6) and *ABCG8* (SEQ ID NO:8) (C). *ABCG5* and *ABCG8* are located on chromosome 2p21 between markers D2S177 and D2S119. (A) *ABCG5* and *ABCG8* are tandemly arrayed in a head-to-head orientation separated by 374 basepairs. *ABCG5* and *ABCG8* are both encoded by 13 exons and each spans ~28 kb. (B) The mutations detected in patients with sitosterolemia (Table 2) are indicated on a schematic model of *ABCG5* (left) and *ABCG8* (right) (C) Predicted amino acid sequence of ABCG5 and ABCG8, which are 651 and 673 residues in length, respectively. Alignment of the inferred amino acid sequences indicates 28% sequence identity and 61% sequence similarity between *ABCG5* and *ABCG8*. Both proteins are predicted to contain six transmembrane segments using the program MEMSAT 2 (Jones, *et al.*, *Biochem.* 33:3038 (1994)). The putative transmembrane segments of each protein are indicated by ~~blue (*ABCG5*) or green (*ABCG8*)~~ cylinders (B) and lines (C). The Walker A motif and Walker B motifs are highlighted ~~in yellow and pink, respectively~~. The ABC signature sequence (C-motif) is indicated ~~in purple~~.

Paragraph **[26]** beginning at line 8 of page 8 has been amended as follows:

[26] FIGURE 3. (A) ABCG8 exon 2 (reverse strand) through ABCG5 exon 2 (forward strand) (SEQ ID NO:9). The four exons are underlined and the conserved regions are in uppercase. The sequence ends in intron 2 of ABCG5 and is in the following order: ABCG8--exon 2 (reverse strand); ABCG8--intron 1 (reverse strand); ABCG8--exon 1 (reverse strand); gap between genes; ABCG5--exon 1 (forward strand); ABCG5--intron 1 (forward strand); ABCG5--exon 2 (forward strand); and ABCG5--intron 2 (forward strand, partial). (B) The sequence between ABCG5 and

ABCG8 in which the control sequences (*e.g.*, bidirectional promoter, *etc.*) reside (SEQ ID NO:10).

Paragraph **[117]** beginning at line 20 of page 33 has been amended as follows:

[117] The particular expression vector used to transport the genetic information into the cell is not particularly critical. Any of the conventional vectors used for expression in eukaryotic or prokaryotic cells may be used. Standard bacterial expression vectors include plasmids such as pBR322 based plasmids, pSKF, pET23D, and fusion expression systems such as GST and LacZ. Epitope tags can also be added to recombinant proteins to provide convenient methods of isolation, e.g., c-myc, HA-tag, 6-His (SEQ ID NO:11) tag, maltose binding protein, VSV-G tag, anti-DYKDDDDK (SEQ ID NO:12) tag, or any such tag, a large number of which are well known to those of skill in the art.

Paragraph **[198]** beginning at line 15 of page 56 has been amended as follows:

[198] Common linkers such as peptides, polyethers, and the like can also serve as tags, and include polypeptide sequences, such as poly-Gly ~~poly-gly~~ sequences of between about 5 and 200 amino acids (SEQ ID NO:13). Such flexible linkers are known to persons of skill in the art. For example, poly(ethelyne glycol) linkers are available from Shearwater Polymers, Inc. Huntsville, Alabama. These linkers optionally have amide linkages, sulfhydryl linkages, or heterofunctional linkages.